



## SEQUENCE LISTING

<110> Presnell, Scott R.  
Burkhead, Steven K.  
Powder, Sarah L.

<120> Human Cytokine Receptor

<130> 99-50

<160> 12

<170> FastSEQ for Windows Version 3.0

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<211> 2255

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (154)...(2229)

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Met Pro Val Pro Trp Phe Leu  
1 5

ctg tcc ttg gca ctg ggc cga agc cca gtg gtc ctt tct ctg gag agg 222  
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Leu Val Gly Pro Gln Asp Ala Thr His Cys Ser Pro Gly Leu Ser Cys  
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cgc ctc tgg gac agt gac ata ctc tgc ctg cct ggg gac atc gtg cct 318  
Arg Leu Trp Asp Ser Asp Ile Leu Cys Leu Pro Gly Asp Ile Val Pro  
40 45 50 55

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OCT 11 2001  
TECH CENTER 1600/2900

AI

gct ccg ggc ccc gtg ctg gcg cct acg cac ctg cag aca gag ctg gtg 366  
Ala Pro Gly Pro Val Leu Ala Pro Thr His Leu Gln Thr Glu Leu Val  
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75 80 85

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Val His Leu Ala Val His Gly His Trp Glu Glu Pro Glu Asp Glu Glu  
90 95 100

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Lys Phe Gly Gly Ala Ala Asp Ser Gly Val Glu Glu Pro Arg Asn Ala  
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Gly Gln Ser Val Gly Ser Val Val Tyr Asp Cys Phe Glu Ala Ala Leu  
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Gly Ser Glu Val Arg Ile Trp Ser Tyr Thr Gln Pro Arg Tyr Glu Lys  
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gaa ctg aac cac aca cag cag ctg cct gcc ctg ccc tgg ctg aac gtg 750  
Glu Leu Asn His Thr Gln Gln Leu Pro Ala Leu Pro Trp Leu Asn Val  
185 190 195

tca gca gat ggt gac aac gtg cat ctg gtt ctg aat gtc tct gag gag 798  
Ser Ala Asp Gly Asp Asn Val His Leu Val Leu Asn Val Ser Glu Glu  
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cag cac ttc ggc ctg tcc ctg tac tgg aat cag gtc cag ggc ccc cca 846  
Gln His Phe Gly Leu Ser Leu Tyr Trp Asn Gln Val Gln Gly Pro Pro  
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 Lys Pro Arg Trp His Lys Asn Leu Thr Gly Pro Gln Ile Ile Thr Leu  
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aac cac aca gac ctg gtt ccc tgc ctc tgt att cag gtg tgg cct ctg 942  
 Asn His Thr Asp Leu Val Pro Cys Leu Cys Ile Gln Val Trp Pro Leu  
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gaa cct gac tcc gtt agg acg aac atc tgc ccc ttc agg gag gac ccc 990  
 Glu Pro Asp Ser Val Arg Thr Asn Ile Cys Pro Phe Arg Glu Asp Pro  
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cgc gca cac cag aac ctc tgg caa gcc gcc cga ctg cga ctg ctg acc 1038  
 Arg Ala His Gln Asn Leu Trp Gln Ala Ala Arg Leu Arg Leu Leu Thr  
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ctg cag agc tgg ctg ctg gac gca ccg tgc tcg ctg ccc gca gaa gcg 1086  
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gca ctg tgc tgg cgg gct ccg ggt ggg gac ccc tgc cag cca ctg gtc 1134  
 Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp Pro Cys Gln Pro Leu Val  
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cca ccg ctt tcc tgg gag aac gtc act gtg gac aag gtt ctc gag ttc 1182  
 Pro Pro Leu Ser Trp Glu Asn Val Thr Val Asp Lys Val Leu Glu Phe  
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 Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala Asp Ser Leu Gly Pro  
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ctc aaa gac gat gtg cta ctg ttg gag aca cga ggc ccc cag gac aac 1326  
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A1  
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Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala Leu Ser Leu Ile Leu	
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Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu Val Gly	
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gcc ctg gcg tcg gcc ctg tgc cag ctg ccg ctg cgc gtg gcc gta gac	1710
Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg Val Ala Val Asp	
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Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp Ala Val  
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cca gac ttc ctg ggg gcc ctg cag cag cct cgc gcc ccg cgt tcc ggg 2094  
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635 640 645

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665 670 675

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<212> PRT

<213> Homo sapiens

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 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr  
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 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys  
 65 70 75 80  
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp  
 85 90 95  
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly  
 100 105 110  
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser  
 115 120 125  
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val  
 130 135 140  
 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr  
 145 150 155 160  
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr  
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 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro  
 180 185 190  
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu  
 195 200 205  
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp  
 210 215 220  
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr  
 225 230 235 240  
 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu  
 245 250 255  
 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile  
 260 265 270  
 Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala  
 275 280 285  
 Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro  
 290 295 300  
 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly  
 305 310 315 320  
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 325 330 335  
 Val Asp Lys Val Leu Glu Phe Pro Leu Leu Lys Gly His Pro Asn Leu  
 340 345 350

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Thr	Arg	Gly	Pro	Gln	Asp	Asn	Arg	Ser	Leu	Cys	Ala	Leu	Glu	Pro	Ser
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Gly	Cys	Thr	Ser	Leu	Pro	Ser	Lys	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu
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Gly	Glu	Tyr	Leu	Leu	Gln	Asp	Leu	Gln	Ser	Gly	Gln	Cys	Leu	Gln	Leu
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Trp	Asp	Asp	Asp	Leu	Gly	Ala	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr
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Ile	His	Lys	Arg	Trp	Ala	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Phe	Ala
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Ala	Ala	Arg	Gly	Arg	Ala	Ala	Leu	Leu	Leu	Tyr	Ser	Ala	Asp	Asp	Ser
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Gly	Phe	Glu	Arg	Leu	Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Cys	Gln	Leu
		500						505					510		
Pro	Leu	Arg	Val	Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	Ala
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Gln	Gly	Pro	Val	Ala	Trp	Phe	His	Ala	Gln	Arg	Arg	Gln	Thr	Leu	Gln
	530					535						540			
Glu	Gly	Gly	Val	Val	Val	Leu	Leu	Phe	Ser	Pro	Gly	Ala	Val	Ala	Leu
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Cys	Ser	Glu	Trp	Leu	Gln	Asp	Gly	Val	Ser	Gly	Pro	Gly	Ala	His	Gly
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Pro	His	Asp	Ala	Phe	Arg	Ala	Ser	Leu	Ser	Cys	Val	Leu	Pro	Asp	Phe
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	595					600						605			
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Phe	Thr	Leu	Pro	Ser	Gln	Leu	Pro	Asp	Phe	Leu	Gly	Ala	Leu	Gln	Gln
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Pro	Arg	Ala	Pro	Arg	Ser	Gly	Arg	Leu	Gln	Glu	Arg	Ala	Glu	Gln	Val
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Ser	Arg	Ala	Leu	Gln	Pro	Ala	Leu	Asp	Ser	Tyr	Phe	His	Pro	Pro	Gly
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Gly Asp Gly Thr  
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sequence of SEQ ID NO:2.

<221> variation  
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gayytntggy	tnmgngtngc	ngtncayyt	gcngtncayg	gncaytggga	rgarccngar	300
gaygargara	arttyggngg	ngcngcngay	wsnggngtng	argarccnmg	naaygcnwsn	360
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gargtncarg	tnccngcngc	nytngtncar	ttyggncarw	sngtnngnws	ngtngtntay	480
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gcngayggng	ayaaygtnc	yytngtnytn	aaygtwnsng	argarcarca	ytyggnytn	660
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&lt;211&gt; 1753

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2)...(1726)

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Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val Pro	
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gct gcc ctt gtg cag ttt ggt cag tct gtg ggc tct gtg gta tat gac	145
Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr Asp	
35 40 45	
tgc ttc gag gct gcc cta ggg agt gag gta cga atc tgg tcc tat act	193
Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr Thr	
50 55 60	
cag ccc agg tac gag aag gaa ctc aac cac aca cag cag ctg cct gcc	241
Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro Ala	
65 70 75 80	

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cag gtc cag ggc ccc cca aaa ccc cgg tgg cac aaa aac ctg act gga Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly 115 120 125	385
ccg cag atc att acc ttg aac cac aca gac ctg gtt ccc tgc ctc tgt Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys 130 135 140	433
att cag gtg tgg cct ctg gaa cct gac tcc gtt agg acg aac atc tgc Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys 145 150 155 160	481
ccc ttc agg gag gac ccc cgc gca cac cag aac ctc tgg caa gcc gcc Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala 165 170 175	529
cga ctg cga ctg ctg acc ctg cag agc tgg ctg ctg gac gca ccg tgc Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys 180 185 190	577
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gac gtg aac agc tcg gag aag ctg cag ctg cag gag tgc ttg tgg gct Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala 225 230 235 240	721
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Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg	
245 250 255	
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Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys	
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Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu	
275 280 285	
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Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp Asp	
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Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His	
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Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala	
325 330 335	
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Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu	
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385 390 395 400	
gta gac ctg tgg agc cgt cgt gaa ctg agc gcg cag ggg ccc gtg gct	1249
Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val Ala	
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tgg ttt cac gcg cag cgg cgc cag acc ctg cag gag ggc ggc gtg gtg	1297
Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val	
420 425 430	
gtc ttg ctc ttc tct ccc ggt gcg gtg gcg ctg tgc agc gag tgg cta	1345
Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp Leu	
435 440 445	
cag gat ggg gtg tcc ggg ccc ggg gcg cac ggc ccg cac gac gcc ttc	1393
Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe	
450 455 460	
cgc gcc tcg ctc agc tgc gtg ctg ccc gac ttc ttg cag ggc cgg gcg	1441
Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala	
465 470 475 480	
ccc ggc agc tac gtg ggg gcc tgc ttc gac agg ctg ctc cac ccg gac	1489
Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp	
485 490 495	
gcc gta ccc gcc ctt ttc cgc acc gtg ccc gtc ttc aca ctg ccc tcc	1537
Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser	
500 505 510	
caa ctg cca gac ttc ctg ggg gcc ctg cag cag cct cgc gcc ccg cgt	1585
Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg	
515 520 525	
tcc ggg cgg ctc caa gag aga gcg gag caa gtg tcc cgg gcc ctt cag	1633
Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln	
530 535 540	
cca gcc ctg gat agc tac ttc cat ccc ccg ggg act ccc gcg ccg gga	1681
Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Thr Pro Ala Pro Gly	
545 550 555 560	
cgc ggg gtg gga cca ggg gcg gga cct ggg gcg ggg gac ggg act	1726
Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr	
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taaataaagg cagacgctgt ttttcta	1753

<211> 575  
 <212> PRT  
 <213> Homo sapiens

<400> 5

Glu	Glu	Pro	Arg	Asn	Ala	Ser	Leu	Gln	Ala	Gln	Val	Val	Leu	Ser	Phe
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Gln	Ala	Tyr	Pro	Thr	Ala	Arg	Cys	Val	Leu	Leu	Glu	Val	Gln	Val	Pro
			20					25					30		
Ala	Ala	Leu	Val	Gln	Phe	Gly	Gln	Ser	Val	Gly	Ser	Val	Val	Tyr	Asp
		35					40					45			
Cys	Phe	Glu	Ala	Ala	Leu	Gly	Ser	Glu	Val	Arg	Ile	Trp	Ser	Tyr	Thr
	50					55					60				
Gln	Pro	Arg	Tyr	Glu	Lys	Glu	Leu	Asn	His	Thr	Gln	Gln	Leu	Pro	Ala
65					70					75				80	
Leu	Pro	Trp	Leu	Asn	Val	Ser	Ala	Asp	Gly	Asp	Asn	Val	His	Leu	Val
			85						90					95	
Leu	Asn	Val	Ser	Glu	Glu	Gln	His	Phe	Gly	Leu	Ser	Leu	Tyr	Trp	Asn
			100						105				110		
Gln	Val	Gln	Gly	Pro	Pro	Lys	Pro	Arg	Trp	His	Lys	Asn	Leu	Thr	Gly
		115					120					125			
Pro	Gln	Ile	Ile	Thr	Leu	Asn	His	Thr	Asp	Leu	Val	Pro	Cys	Leu	Cys
	130					135					140				
Ile	Gln	Val	Trp	Pro	Leu	Glu	Pro	Asp	Ser	Val	Arg	Thr	Asn	Ile	Cys
145					150					155				160	
Pro	Phe	Arg	Glu	Asp	Pro	Arg	Ala	His	Gln	Asn	Leu	Trp	Gln	Ala	Ala
			165						170					175	
Arg	Leu	Arg	Leu	Leu	Thr	Leu	Gln	Ser	Trp	Leu	Leu	Asp	Ala	Pro	Cys
			180					185					190		
Ser	Leu	Pro	Ala	Glu	Ala	Ala	Leu	Cys	Trp	Arg	Ala	Pro	Gly	Gly	Asp
		195					200					205			
Pro	Cys	Gln	Pro	Leu	Val	Pro	Pro	Leu	Ser	Trp	Glu	Asn	Val	Thr	Val
	210					215					220				
Asp	Val	Asn	Ser	Ser	Glu	Lys	Leu	Gln	Leu	Gln	Glu	Cys	Leu	Trp	Ala
225					230					235				240	
Asp	Ser	Leu	Gly	Pro	Leu	Lys	Asp	Asp	Val	Leu	Leu	Leu	Glu	Thr	Arg
			245						250					255	
Gly	Pro	Gln	Asp	Asn	Arg	Ser	Leu	Cys	Ala	Leu	Glu	Pro	Ser	Gly	Cys
		260					265						270		
Thr	Ser	Leu	Pro	Ser	Lys	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	Glu
		275					280					285			
Tyr	Leu	Leu	Gln	Asp	Leu	Gln	Ser	Gly	Gln	Cys	Leu	Gln	Leu	Trp	Asp
	290					295						300			

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Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His
305          310          315          320
Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala
          325          330          335
Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly Trp Leu
          340          345          350
Arg Leu Leu Lys Gln Asp Val Arg Ser Gly Ala Ala Ala Arg Gly Arg
          355          360          365
Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu
          370          375          380
Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg Val Ala
385          390          395          400
Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val Ala
          405          410          415
Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val
          420          425          430
Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp Leu
          435          440          445
Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe
          450          455          460
Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala
465          470          475          480
Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp
          485          490          495
Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser
          500          505          510
Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg
          515          520          525
Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln
          530          535          540
Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Thr Pro Ala Pro Gly
545          550          555          560
Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr
          565          570          575

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<210> 6

<211> 1725

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate sequence encodes the amino acid  
sequence of SEQ ID NO:5.

<221> variation  
 <222> (1)...(1725)  
 <223> N is any nucleotide.

<221> misc\_feature  
 <222> (1)...(1725)  
 <223> n = A,T,C or G

<400> 6

AI  
conf.

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acngcnmgnt	gygtntytyt	ngargtnear	gtncngcng	cnytngtnc	rttyggncar	120
wsngtnggnw	sngtngnta	ygaytgyty	gargcngcny	tnngnwsnga	rgtnmgnath	180
tggwsntaya	cncarccnm	ntaygaraar	garytnaayc	ayacncarca	rytnccngcn	240
ytnccntggy	tnaaygtnws	ngcngayggn	gayaaygtnc	ayytngtnyt	naaygtnwsn	300
gargarcarc	ayttyggnyt	nwsnyntay	tggaaycarg	tnccargncc	nccnaarccn	360
mgntggcaya	araayytnc	nggnccncar	athathacny	tnaaycayac	ngayytngtn	420
ccntggytnt	gyathcargt	ntggccnytn	garccngayw	sngtnmgnac	naayathtgy	480
ccnttymgng	argayccnm	ngcncaycar	aayytntggc	argcngcnmg	nytnmgnytn	540
ytnacnytn	arwsntggyt	nytnngaycn	ccntgywsny	tnccngcnga	rgcngcnytn	600
tgytggmgng	cncngggng	ngayccntgy	carccnytn	tnccncnytn	nwsntgggar	660
aaygtnacng	tnngaygtnaa	ywsnwsngar	aarytnccary	tnccargartg	yytntgggcn	720
gaywsnytn	gncnytnaa	rgaygaygt	ytnytnytn	aracnmngng	nccncargay	780
aaymgnwsny	tnngygcnytn	ngarccnwsn	ggntgyacnw	snytnccnws	naargcnwsn	840
acnmngcng	cnmngnytn	ngartayytn	ytnccargay	tnccarwsngg	ncartgyytn	900
carytnntggg	aygaygayt	nggngcnytn	tgggcntgyc	cnatggayaa	rtayathcay	960
aarmgntggg	cnytngtntg	gytnccntgy	ytnytnnttyg	cngcngcnytn	nwsnytnath	1020
ytnytnytna	araargayca	ygcnaarggn	tggynmngny	tnytnaarca	rgaygtmngn	1080
wsnggngcng	cngcnmgngg	nmngngcngcn	ytnytnytn	aywsngcnga	ygaywsnggn	1140
ttygarmgny	tngtnggngc	nytnngcnwsn	gcnytnntgyc	arytnccnytn	nmngngtnngcn	1200
gtngayytn	ggwsnmngm	ngarytnwsn	gcncarggnc	cngtnccntg	gttycaygc	1260
carmgnmngc	aracnytnca	rgarggnggn	gtngtngtny	tnytnnttyws	nccnggngcn	1320
gtngcnytn	gywsngartg	gytnccargay	ggngtnwsng	gnccnggngc	ncayggncn	1380
caygaygcnt	tymngncnws	nytnwsntgy	gtnytnccng	ayttyytnca	rggnmngcn	1440
ccnggnwsnt	aygtnggngc	ntgyttygay	mgnytnytn	ayccngaygc	ngtnccngcn	1500
ytnnttymgna	cngtnccngt	nttyacnytn	ccnwsncary	tnccngaytt	yytnnggngcn	1560
ytnccarcarc	cnmngncncc	nmgnwsnggn	mgnytnccarg	armngngcnga	rcargtnwsn	1620
mgngcnytn	arccngcnytn	ngaywsntay	ttycayccnc	cnggnacncc	ngcncngggn	1680
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 <211> 16  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker.

<400> 7

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<210> 8

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 8

cggcgtggtg gtcttgctct t

21

<210> 9

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer.

<400> 9

tcccgtcccc cgccccaggt c

21

<210> 10

<211> 688

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric Zcytor14 protein.

<400> 10

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1 5 10 15



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 20 25 30  
 Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys  
 35 40 45  
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr  
 50 55 60  
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys  
 65 70 75 80  
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp  
 85 90 95  
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly  
 100 105 110  
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser  
 115 120 125  
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val  
 130 135 140  
 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr  
 145 150 155 160  
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr  
 165 170 175  
 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro  
 180 185 190  
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu  
 195 200 205  
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp  
 210 215 220  
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr  
 225 230 235 240  
 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu  
 245 250 255  
 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile  
 260 265 270  
 Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala  
 275 280 285  
 Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro  
 290 295 300  
 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly  
 305 310 315 320  
 Asp Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr  
 325 330 335  
 Val Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp  
 340 345 350

Ala	Asp	Ser	Leu	Gly	Pro	Leu	Lys	Asp	Asp	Val	Leu	Leu	Leu	Glu	Thr
	355						360				365				
Arg	Gly	Pro	Gln	Asp	Asn	Arg	Ser	Leu	Cys	Ala	Leu	Glu	Pro	Ser	Gly
	370					375					380				
Cys	Thr	Ser	Leu	Pro	Ser	Lys	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly
385					390					395				400	
Glu	Tyr	Leu	Leu	Gln	Asp	Leu	Gln	Ser	Gly	Gln	Cys	Leu	Gln	Leu	Trp
			405					410					415		
Asp	Asp	Asp	Leu	Gly	Ala	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	Ile
			420					425				430			
His	Lys	Arg	Trp	Ala	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Phe	Ala	Ala
	435						440					445			
Ala	Leu	Ser	Leu	Ile	Leu	Leu	Leu	Lys	Lys	Asp	His	Ala	Lys	Gly	Trp
	450					455					460				
Leu	Arg	Leu	Leu	Lys	Gln	Asp	Val	Arg	Ser	Gly	Ala	Ala	Ala	Arg	Gly
465				470						475				480	
Arg	Ala	Ala	Leu	Leu	Tyr	Ser	Ala	Asp	Asp	Ser	Gly	Phe	Glu	Arg	
			485					490				495			
Leu	Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Cys	Gln	Leu	Pro	Leu	Arg	Val
			500					505				510			
Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	Ala	Gln	Gly	Pro	Val
	515						520					525			
Ala	Trp	Phe	His	Ala	Gln	Arg	Arg	Gln	Thr	Leu	Gln	Glu	Gly	Gly	Val
	530					535					540				
Val	Val	Leu	Leu	Phe	Ser	Pro	Gly	Ala	Val	Ala	Leu	Cys	Ser	Glu	Trp
545				550						555				560	
Leu	Gln	Asp	Gly	Val	Ser	Gly	Pro	Gly	Ala	His	Gly	Pro	His	Asp	Ala
			565					570				575			
Phe	Arg	Ala	Ser	Leu	Ser	Cys	Val	Leu	Pro	Asp	Phe	Leu	Gln	Gly	Arg
			580					585				590			
Ala	Pro	Gly	Ser	Tyr	Val	Gly	Ala	Cys	Phe	Asp	Arg	Leu	Leu	His	Pro
	595						600					605			
Asp	Ala	Val	Pro	Ala	Leu	Phe	Arg	Thr	Val	Pro	Val	Phe	Thr	Leu	Pro
	610					615						620			
Ser	Gln	Leu	Pro	Asp	Phe	Leu	Gly	Ala	Leu	Gln	Gln	Pro	Arg	Ala	Pro
625				630						635				640	
Arg	Ser	Gly	Arg	Leu	Gln	Glu	Arg	Ala	Glu	Gln	Val	Ser	Arg	Ala	Leu
			645					650				655			
Gln	Pro	Ala	Leu	Asp	Ser	Tyr	Phe	His	Pro	Pro	Gly	Thr	Pro	Ala	Pro
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Gly	Arg	Gly	Val	Gly	Pro	Gly	Ala	Gly	Pro	Gly	Ala	Gly	Asp	Gly	Thr
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<210> 11  
 <211> 705  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Chimeric Zcytor14 protein.

<400> 11

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 Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys  
 35 40 45  
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr  
 50 55 60  
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys  
 65 70 75 80  
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp  
 85 90 95  
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly  
 100 105 110  
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser  
 115 120 125  
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val  
 130 135 140  
 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr  
 145 150 155 160  
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr  
 165 170 175  
 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro  
 180 185 190  
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu  
 195 200 205  
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp  
 210 215 220  
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr  
 225 230 235 240  
 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu  
 245 250 255  
 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile  
 260 265 270

AI  
 cont

Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala  
 275 280 285  
 Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro  
 290 295 300  
 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly  
 305 310 315 320  
 Asp Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr  
 325 330 335  
 Val Asp Lys Val Leu Glu Phe Pro Leu Leu Lys Gly His Pro Asn Leu  
 340 345 350  
 Cys Val Gln Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu  
 355 360 365  
 Trp Ala Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu  
 370 375 380  
 Thr Arg Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser  
 385 390 395 400  
 Gly Cys Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu  
 405 410 415  
 Gly Glu Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu  
 420 425 430  
 Trp Asp Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr  
 435 440 445  
 Ile His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala  
 450 455 460  
 Ala Ala Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly  
 465 470 475 480  
 Trp Leu Arg Leu Leu Lys Gln Asp Val Arg Ser Gly Ala Ala Ala Arg  
 485 490 495  
 Gly Arg Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu  
 500 505 510  
 Arg Leu Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg  
 515 520 525  
 Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro  
 530 535 540  
 Val Ala Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly  
 545 550 555 560  
 Val Val Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu  
 565 570 575  
 Trp Leu Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp  
 580 585 590  
 Ala Phe Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly  
 595 600 605

AI  
 conf.

Arg Ala Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His  
 610 615 620  
 Pro Asp Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu  
 625 630 635 640  
 Pro Ser Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala  
 645 650 655  
 Pro Arg Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala  
 660 665 670  
 Leu Gln Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Thr Pro Ala  
 675 680 685  
 Pro Gly Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly  
 690 695 700  
 Thr  
 705

<210> 12  
 <211> 675  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Chimeric Zcytor14 protein.

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 Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys  
 35 40 45  
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr  
 50 55 60  
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys  
 65 70 75 80  
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp  
 85 90 95  
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly  
 100 105 110  
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser  
 115 120 125  
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val  
 130 135 140

A1  
 cont.

Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr  
 145 150 155 160  
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr  
 165 170 175  
 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro  
 180 185 190  
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu  
 195 200 205  
 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp  
 210 215 220  
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr  
 225 230 235 240  
 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu  
 245 250 255  
 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile  
 260 265 270  
 Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala  
 275 280 285  
 Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro  
 290 295 300  
 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly  
 305 310 315 320  
 Asp Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr  
 325 330 335  
 Val Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp  
 340 345 350  
 Ala Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr  
 355 360 365  
 Arg Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly  
 370 375 380  
 Cys Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly  
 385 390 395 400  
 Glu Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp  
 405 410 415  
 Asp Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile  
 420 425 430  
 His Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala  
 435 440 445  
 Ala Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Ala Ala  
 450 455 460  
 Ala Arg Gly Arg Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly  
 465 470 475 480

A1  
 cont.

Phe Glu Arg Leu Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro  
 485 490 495  
 Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln  
 500 505 510  
 Gly Pro Val Ala Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu  
 515 520 525  
 Gly Gly Val Val Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys  
 530 535 540  
 Ser Glu Trp Leu Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro  
 545 550 555 560  
 His Asp Ala Phe Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu  
 565 570 575  
 Gln Gly Arg Ala Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu  
 580 585 590  
 Leu His Pro Asp Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe  
 595 600 605  
 Thr Leu Pro Ser Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro  
 610 615 620  
 Arg Ala Pro Arg Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser  
 625 630 635 640  
 Arg Ala Leu Gln Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Thr  
 645 650 655  
 Pro Ala Pro Gly Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly  
 660 665 670  
 Asp Gly Thr  
 675

A1  
 cont.